

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SOPPET, DANIEL R.
RUBEN, STEVEN M.
- (ii) TITLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: US
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/042,855
 - (B) FILING DATE: 28-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEFFE, ERIC K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0620001
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 233..1423
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide

(B) LOCATION: 233..328

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 329..1423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGCGGCAC GGCAGCAGCG GCAACAAGTG CCGGACTAGC AGAGCCAAGC CGGAGCAGTC	60
CCTGCCGCGG ACACCGCCGG GCCGCCCGTC CGGGGCGCCG CGCATGGAGC GTGAGCTGCG	120
GCGGTCGCGG GGGCTGAGCC GCGCGGAGCG CCGGGACGTG GATGTGGCCG CGATCTCCCG	180
CCCTTGCCCC CGCCCCGCGG AGCTGGAGCT GCTCCCGGAC AAGATATGAG AA ATG	235
	Met
	-32
AGT GTT GGA CGT CGA AGA ATA AAG TTG TTG GGT ATC CTG ATG ATG GCA	283
Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met Ala	
-30 -25 -20	
AAT GTC TTC ATT TAT TTT ATT ATG GAA GTC TCC AAA AGC AGT AGC CAA	331
Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser Gln	
-15 -10 -5 1	
GAA AAA AAT GGA AAA GGG GAA GTA ATA ATA CCC AAA GAG AAG TTC TGG	379
Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe Trp	
5 10 15	
AAG ATA TCT ACC CCT CCC GAG GCA TAC TGG AAC CGA GAG CAA GAG AAG	427
Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu Lys	
20 25 30	
CTG AAC CGG CAG TAC AAC CCC ATC CTG AGC ATG CTG ACC AAC CAG ACG	475
Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln Thr	
35 40 45	
GGG GAG GCG GGC AGG CTC TCC AAT ATA AGC CAT CTG AAC TAC TGC GAA	523
Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys Glu	
50 55 60 65	
CCT GAC CTG AGG GTC ACG TCG GTG GTT ACG GGT TTT AAC AAC TTG CCG	571
Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu Pro	
70 75 80	
GAC AGA TTT AAA GAC TTT CTG CTG TAT TTG AGA TGC CGC AAT TAT TCA	619
Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr Ser	
85 90 95	
CTG CTT ATA GAT CAG CCG GAT AAG TGT GCA AAG AAA CCT TTC TTG TTG	667
Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu Leu	
100 105 110	
CTG GCG ATT AAG TCC CTC ACT CCA CAT TTT GCC AGA AGG CAA GCA ATC	715
Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala Ile	
115 120 125	
CGG GAA TCC TGG GGC CAA GAA AGC AAC GCA GGG AAC CAA ACG GTG GTG	763
Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val Val	
130 135 140 145	

CGA	GTC	TTC	CTG	CTG	GGC	CAG	ACA	CCC	CCA	GAG	GAC	AAC	CAC	CCC	GAC	811
Arg	Val	Phe	Leu	Leu	Gly	Gln	Thr	Pro	Pro	Glu	Asp	Asn	His	Pro	Asp	
			150					155						160		
CTT	TCA	GAT	ATG	CTG	AAA	TTT	GAG	AGT	GAG	AAG	CAC	CAA	GAC	ATT	CTT	859
Leu	Ser	Asp	Met	Leu	Lys	Phe	Glu	Ser	Glu	Lys	His	Gln	Asp	Ile	Leu	
			165					170					175			
ATG	TGG	AAC	TAC	AGA	GAC	ACT	TTC	TTC	AAC	TTG	TCT	CTG	AAG	GAA	GTG	907
Met	Trp	Asn	Tyr	Arg	Asp	Thr	Phe	Phe	Asn	Leu	Ser	Leu	Lys	Glu	Val	
		180					185					190				
CTG	TTT	CTC	AGG	TGG	GTA	AGT	ACT	TCC	TGC	CCA	GAC	ACT	GAG	TTT	GTT	955
Leu	Phe	Leu	Arg	Trp	Val	Ser	Thr	Ser	Cys	Pro	Asp	Thr	Glu	Phe	Val	
	195					200					205					
TTC	AAG	GGC	GAT	GAC	GAT	GTT	TTT	GTG	AAC	ACC	CAT	CAC	ATC	CTG	AAT	1003
Phe	Lys	Gly	Asp	Asp	Asp	Val	Phe	Val	Asn	Thr	His	His	Ile	Leu	Asn	
210				215					220					225		
TAC	TTG	AAT	AGT	TTA	TCC	AAG	ACC	AAA	GCC	AAA	GAT	CTC	TTC	ATA	GGT	1051
Tyr	Leu	Asn	Ser	Leu	Ser	Lys	Thr	Lys	Ala	Lys	Asp	Leu	Phe	Ile	Gly	
			230					235						240		
GAT	GTG	ATC	CAC	AAT	GCT	GGA	CCT	CAT	CGG	GAT	AAG	AAG	CTG	AAG	TAC	1099
Asp	Val	Ile	His	Asn	Ala	Gly	Pro	His	Arg	Asp	Lys	Lys	Leu	Lys	Tyr	
			245				250						255			
TAC	ATC	CCA	GAA	GTT	GTT	TAC	TCT	GGC	CTC	TAC	CCA	CCC	TAT	GCA	GGG	1147
Tyr	Ile	Pro	Glu	Val	Val	Tyr	Ser	Gly	Leu	Tyr	Pro	Pro	Tyr	Ala	Gly	
		260					265					270				
GGA	GGG	GGG	TTC	CTC	TAC	TCC	GGC	CAC	CTG	GCC	CTG	AGG	CTG	TAC	CAT	1195
Gly	Gly	Gly	Phe	Leu	Tyr	Ser	Gly	His	Leu	Ala	Leu	Arg	Leu	Tyr	His	
	275					280					285					
ATC	ACT	GAC	CAG	GTC	CAT	CTC	TAC	CCC	ATT	GAT	GAC	GTT	TAT	ACT	GGA	1243
Ile	Thr	Asp	Gln	Val	His	Leu	Tyr	Pro	Ile	Asp	Asp	Val	Tyr	Thr	Gly	
290					295				300						305	
ATG	TGC	CTT	CAG	AAA	CTC	GGC	CTC	GTT	CCA	GAG	AAA	CAC	AAA	GGC	TTC	1291
Met	Cys	Leu	Gln	Lys	Leu	Gly	Leu	Val	Pro	Glu	Lys	His	Lys	Gly	Phe	
			310					315						320		
AGG	ACA	TTT	GAT	ATC	GAG	GAG	AAA	AAC	AAA	AAT	AAC	ATC	TGC	TCC	TAT	1339
Arg	Thr	Phe	Asp	Ile	Glu	Glu	Lys	Asn	Lys	Asn	Asn	Ile	Cys	Ser	Tyr	
			325					330					335			
GTA	GAT	CTG	ATG	TTA	GTA	CAT	AGT	AGA	AAA	CCT	CAA	GAG	ATG	ATT	GAT	1387
Val	Asp	Leu	Met	Leu	Val	His	Ser	Arg	Lys	Pro	Gln	Glu	Met	Ile	Asp	
		340					345					350				
ATT	TGG	TCT														

TTTTTATGGA TGATATGGCA GGATGATTGG TTCTGATCTT ACCGGCTAGT GGTCATTTTT	1673
AAAAAACTTG TACCCCTCTTA TCTGAAATCC TGTTTCTGGA ATTTGGCCAT TTTAAGTGAT	1733
TTTGTGTTGCC CTCTTCTATA ATATTCCTAC TTCCCATAAAT AATGACTGAT TTATTTGTAA	1793
TTCAGGTATT TATAAACCTA TTGGCTACAA AGACTTTGTT AAACATTATC CAGTGGTTTT	1853
CGTGAAATGG AATTATGTTT ATTTTATGGA GATTTGGGTA AATTTTAAAT TGTCTAGAAA	1913
ACTGAAATTT CAGTTGTCAG TTGTGGAATT CAGTTTTTCA ATTGTGGAAA TTCCTGCCA	1973
CCCCAACAGT ATTTTGTGT GTTAATTAAT TTTGCAAAAT GAGAATCATG GTGTGACACT	2033
CATCTAATTT ATCTTGTTGT GATGTTATGG TCATAATAAG GAGAAAGAGG GTTTAATTTT	2093
TCTTGATTTT GGTTTCCTGG TGGTATCATA GTGTAATTTT AGTATTTGAA AATCAGTGTG	2153
ATTCCTTAAT GGCCAACTGA AGATTGAATT GCCGCTAACA ACCATATCGT GTTAGTGAAT	2213
TTTCAATATG GACCAGGAAG GCATATGTAT TTTGAACTTG AGTGAAAAGG TTGAAGTTAC	2273
AGACTTTTGC ATAGATGGTT TGTCATTTA AAATTCCAGA ATTTATTATT GCCATATTTT	2333
CACATGCTGC TTATACAAGA TTATTATTGA GTAGTAACTG TTCCCTGTCT ATGTAGAAGT	2393
GCCTGTGTTT TTATTTATTG TTCCAGATCA AAGACCAAAA CATTTTCTTA AATATCTCTT	2453
ATGTAATATT TTATTTGTAT ACAGTGTTGT TGATGAAATA TTAACTAGA GCATGATATT	2513
TTAAATGTTA AGGTGTAACA TATGTTAAAT AAACTGTTA TTTTGAATT TTAAATTTG	2573
TTTTTTGGGG GTATGAACTA CTAGAGTTTA AAATTCTGCC AAATATTAC TTATATGTAC	2633
TATTGTGTAA CATACTTCT TGAAATATTT TTGTTTATAG AATTGAAGGT TCTTATCAGA	2693
TGGGATACTG GGGATTATAA ACAATGGAAA TAAAGCCACT GTATTTTAA AA	2745

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met	
-32 -30 -25 -20	
Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser	
-15 -10 -5	
Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe	
1 5 10 15	
Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu	
20 25 30	

Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln
 35 40 45
 Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys
 50 55 60
 Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu
 65 70 75 80
 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
 85 90 95
 Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu
 100 105 110
 Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala
 115 120 125
 Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val
 130 135 140
 Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro
 145 150 155 160
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile
 165 170 175
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
 180 185 190
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe
 195 200 205
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
 210 215 220
 Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile
 225 230 235 240
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
 245 250 255
 Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala
 260 265 270
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr
 275 280 285
 His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
 290 295 300
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
 305 310 315 320
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser
 325 330 335
 Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
 340 345 350
 Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
 355 360 365

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Ser Lys His Arg Lys Leu Leu Leu Arg Cys Leu Leu Val Leu Pro
 1 5 10 15
 Leu Ile Leu Leu Val Asp Tyr Cys Gly Leu Leu Thr His Leu His Glu
 20 25 30
 Leu Asn Phe Glu Arg His Phe His Tyr Pro Leu Asn Asp Asp Thr Gly
 35 40 45
 Ser Gly Ser Ala Ser Ser Gly Leu Asp Lys Phe Ala Tyr Leu Arg Val
 50 55 60
 Pro Ser Phe Thr Ala Glu Val Pro Val Asp Gln Pro Ala Arg Leu Thr
 65 70 75 80
 Met Leu Ile Lys Ser Ala Val Gly Asn Ser Arg Arg Arg Glu Ala Ile
 85 90 95
 Arg Arg Thr Trp Gly Tyr Glu Gly Arg Phe Ser Asp Val His Leu Arg
 100 105 110
 Arg Val Phe Leu Leu Gly Thr Ala Glu Asp Ser Glu Lys Asp Val Ala
 115 120 125
 Trp Glu Ser Arg Glu His Gly Asp Ile Leu Gln Ala Asp Phe Thr Asp
 130 135 140
 Ala Tyr Phe Asn Asn Thr Leu Lys Thr Met Leu Gly Met Arg Trp Ala
 145 150 155 160
 Ser Glu Gln Phe Asn Arg Ser Glu Phe Tyr Leu Phe Val Asp Asp Asp
 165 170 175
 Tyr Tyr Val Ser Ala Lys Asn Val Leu Lys Phe Leu Gly Arg Gly Arg
 180 185 190
 Gln Ser His Gln Pro Glu Leu Leu Phe Ala Gly His Val Phe Gln Thr
 195 200 205
 Ser Pro Leu Arg His Lys Phe Ser Lys Trp Tyr Val Ser Leu Glu Glu
 210 215 220
 Tyr Pro Phe Asp Arg Trp Pro Pro Tyr Val Thr Ala Gly Ala Phe Ile
 225 230 235 240
 Leu Ser Gln Lys Ala Leu Arg Gln Leu Tyr Ala Ala Ser Val His Leu
 245 250 255

Pro Leu Phe Arg Phe Asp Asp Val Tyr Leu Gly Ile Val Ala Leu Lys
 260 265 270
 Ala Gly Ile Ser Leu Gln His Cys Asp Asp Phe Arg Phe His Arg Pro
 275 280 285
 Ala Tyr Lys Gly Pro Asp Ser Tyr Ser Ser Val Ile Ala Ser His Glu
 290 295 300
 Phe Gly Asp Pro Glu Glu Met Thr Arg Val Trp Asn Glu Cys Arg Ser
 305 310 315 320
 Ala Asn Tyr

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGATCC CAAGAAAAAA ATGGAAAAGG G

31

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTGTCTAGA TATCTATTTT AGCATTTTA

29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCCGGATCC GCCATCATGA GTGTTGGACG TCGAAGAAT

39

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATTGTCTAGA ATTTTAAGCG TAGTCTGGGA CGTCGTATGG GTAGCATTTT AAATGAGCAC

60

TCTG

64

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT

60

GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATCCACAC AACATACGAG

120

CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG

180

CGTTGCGCTC ACTGCCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA

240

TCGGCCAACG CGCGGGGAGA GGCAGTTTGC GTATTGGGCG CTCTTCGCT TCCTCGCTCA

300

CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCAGAGCGT ATCAGCTCAC TCAAAGGCGG

360

TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC

420

AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC

480

CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC

540

TATAAAGATA CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC

600

TGCCGCTTAC CGGATACCTG TCCGCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA

660

GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTTC CTCCAAGCTG GGCTGTGTGC

720

ACGAACCCCC	CGTTCAGCCC	GACCGCTGCG	CCTTATCCGG	TAACTATCGT	CTTGAGTCCA	780
ACCCGGTAAG	ACACGACTTA	TCGCCACTGG	CAGCAGCCAC	TGGTAACAGG	ATTAGCAGAG	840
CGAGGTATGT	AGGCGGTGCT	ACAGAGTTCT	TGAAGTGGTG	GCCTAACTAC	GGCTACACTA	900
GAAGAACAGT	ATTTGGTATC	TGCGCTCTGC	TGAAGCCAGT	TACCTTCGGA	AAAAGAGTTG	960
GTAGCTCTTG	ATCCGGCAAA	CAAACCACCG	CTGGTAGCGG	TGGTTTTTTT	GTTTGCAAGC	1020
AGCAGATTAC	GCGCAGAAAA	AAAGGATCTC	AAGAAGATCC	TTTGATCTTT	TCTACGGGGT	1080
CTGACGCTCA	GTGGAACGAA	AACTCACGTT	AAGGGATTTT	GGTCATGAGA	TTATCGTCGA	1140
CAATTCGCGC	GCGAAGGCGA	AGCGGCATGC	ATTTACGTTG	ACACCATCGA	ATGGTGCAAA	1200
ACCTTTCGCG	GTATGGCATG	ATAGCGCCCG	GAAGAGAGTC	AATTCAGGGT	GGTGAATGTG	1260
AAACCAGTAA	CGTTATACGA	TGTCGCAGAG	TATGCCGGTG	TCTCTTATCA	GACCGTTTCC	1320
CGCGTGGTGA	ACCAGGCCAG	CCACGTTTCT	GCGAAAACGC	GGGAAAAAGT	GGAAGCGGCG	1380
ATGGCGGAGC	TGAATTACAT	TCCCAACCGC	GTGGCACAAC	AACTGGCGGG	CAAACAGTCG	1440
TTGCTGATTG	GCGTTGCCAC	CTCCAGTCTG	GCCCTGCACG	CGCCGTCGCA	AATTGTCGCG	1500
GCGATTAAAT	CTCGCGCCGA	TCAACTGGGT	GCCAGCGTGG	TGGTGTGAT	GGTAGAACGA	1560
AGCGGCGTCG	AAGCCTGTAA	AGCGGCGGTG	CACAATCTTC	TCGCGCAACG	CGTCAGTGGG	1620
CTGATCATT	ACTATCCGCT	GGATGACCAG	GATGCCATTG	CTGTGGAAGC	TGCCTGCACT	1680
AATGTTCCGG	CGTTATTTCT	TGATGTCTCT	GACCAGACAC	CCATCAACAG	TATTATTTTC	1740
TCCCATGAAG	ACGGTACGCG	ACTGGGCGTG	GAGCATCTGG	TCGCATTGGG	TCACCAGCAA	1800
ATCGCGCTGT	TAGCGGGCCC	ATTAAGTTCT	GTCTCGGCGC	GTCTGCGTCT	GGCTGGCTGG	1860
CATAAATATC	TCACTCGCAA	TCAAATTCAG	CCGATAGCGG	AACGGGAAGG	CGACTGGAGT	1920
GCCATGTCCG	GTTTTCAACA	AACCATGCAA	ATGCTGAATG	AGGGCATCGT	TCCCACTGCG	1980
ATGCTGGTTG	CCAACGATCA	GATGGCGCTG	GGCGCAATGC	GCGCCATTAC	CGAGTCCGGG	2040
CTGCGCGTTG	GTGCGGATAT	CTCGGTAGTG	GGATACGACG	ATACCGAAGA	CAGCTCATGT	2100
TATATCCCGC	CGTTAACCAC	CATCAAACAG	GATTTTCGCC	TGCTGGGGCA	AACCAGCGTG	2160
GACCGCTTGC	TGCAACTCTC	TCAGGGCCAG	GCGGTGAAGG	GCAATCAGCT	GTTGCCCGTC	2220
TCACTGGTGA	AAAGAAAAAC	CACCCTGGCG	CCCAATACGC	AAACCGCCTC	TCCCCGCGCG	2280
TTGGCCGATT	CATTAATGCA	GCTGGCACGA	CAGGTTTCCC	GACTGGAAAG	CGGGCAGTGA	2340
GCGCAACGCA	ATTAATGTAA	GTTAGCGCGA	ATTGTCGACC	AAAGCGGCCA	TCGTGCCTCC	2400
CCACTCCTGC	AGTTCGGGGG	CATGGATGCG	CGGATAGCCG	CTGCTGGTTT	CCTGGATGCC	2460
GACGGATTTG	CACTGCCGGT	AGAACTCCGC	GAGGTGCTCC	AGCCTCAGGC	AGCAGCTGAA	2520
CCAACTCGCG	AGGGGATCGA	GCCCCGGGTG	GGCGAAGAAC	TCCAGCATGA	GATCCCCGCG	2580

CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGGC GTCGCTTGGT CGGTCATTTC	2700
GAACCCAGAG GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760
GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTTC GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG	2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TCGCGCCTT GAGCCTGGCG	3000
AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTCG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTCAATC ATGCGAAACG ATCCTCATCC TGTCCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTTGCGC TTGCGTTTTT CCTTGTCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC	3840
CCTGAGTGCT TGCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTACAC ATTAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC 60
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG 112

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAAAATACAG TGGCTTTATT TCCATTGTTT ATAGTCCCCA GTATCCCATC TGATAAGAAC 60
CTTCAATTCT ATAAACAAAA ATATTTCAAG AAAGTATGTT ACACAATAGT ACATATAAGT 120
AATAGTTTGG CAGAATTTTA AACTCTAGTA GTTCATACCC CCAAAAAACA AATTTTAAAN 180
TTCAAAAATA ACAGTTTTAT TTAACATATG TTACACCTTA ACATTTAAAA TATCATGCTC 240
TAGTTAAATA TTTCATCAAC AACACTGTAT ACANNTAAAA TATTACATAA AATATATTT 299

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTGCCAGA AGGCAAGCAA TCCGGGAATC CTGGGGCCAA GAAAGCAACG CAGGGAACCA 60
AACGGTGGTG CGAGTNTTCC TGCTGGGCCA GACACCCCCA GAGGACAACC ACCCCGACCT 120
TTCAGATATG CTGAAATTTG AGAGTGAGAA GCACCAAGAC ATTCTTATGT GGAACTACAG 180
AGACACTTTN TTCAACTTGT CTCTGAAGGA AGTGCTGTTT CTNAGGTGGG TAAGTACTTC 240
CTGCCCAGAC ACTGAGTTTG TTTTCAAGGG CGATGACGAT GT 282

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGGCCAGA AGGCAAGCAA TCCGGGAATC CTGGGGCCAA GAAAGCAACG CAGGGAACCA	60
AACGGTGGTG CGAGTNTTCC TGCTGGGCCA GACACCCCA GAGGACAACC ACCCCGACCT	120
TTCAGATATG CTGAAATTTG AGAGTNAGAA GCACCAAGAC ATTCTTATGT GGAACACAG	180
AGACACTTTC TTCAACTTGT CTCTGAAGGA AGTGCTGTTT CTCAGGTGGG TAAGTACTTC	240
CTGCCCAGAC ACTGAGTTTG TTTTCA	266

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTGCAAAAT GAGAATCATG GTGTGACACT CATCTAATTT ATCTTGTGTG GATGTTATGG	60
TCATAATAAG GAGAAANAGG GTTTAATTTT NCTTGATTTT GGTTTCCTGG TGGTATCATA	120
GTGTAATTTT AGTATTTGAA AATCAGTGTG ATTCCTTAAT GGCCAACTGA AGATTGAATT	180
GCCGCTAACA ACCATATCGT GTTAGTGAAT TTNCAATATG GACCAGGAAG GCATATGTAT	240
TTTGAACCTCG GAGTGAAAAG GTTGGAAGTT ACAGACTTTT TGGCATAGGT GGGTTTGGTC	300
CAATTTTAAA ATTCCCGAAT TTATTNNTTG NCNNTTNTTN CACATGGGNG GTTATTACAG	360
G	361

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTGTTGGGTA TCCTGATGAT GGCAAATGTC TTCATTTATT TTATTATGGA AGTCTCCAAA	60
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AGCAGTAGCC AAGAAAAAAA TGGAAAAGGG GAAGTAATAA TACCCAAAGA GAAGTTCTGG	120
AAGATATCTA CCCCTCCCGA GGCATACTNG AACCGAGAGC AAGAGAAGCT GAACCGGCAG	180
TACAACCCCA TCCTGAGCAT GCTGACCAAC CAGACGGGGG AGGCGGGCAG GCTCTCCAAT	240
ATAAGNCATC TGAACACT	259

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAAAATACAG TGGCTTTATT TCCATTGTTT ATAGTCCCCA GSTATCCCATC TGATAAGAAC	60
CTNCAATTCT ATAAACAAAA ATATTTCAAG AAAGTATGTT ACACAATAGT ACATATAAGT	120
AATAGTTTGG CAGAATTTTA AACTCTAGTA GTTCATACCC CCAAAAAACA AATTTTAAAA	180
TTCAAAAATA ACAGT	195

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTATAATATT CCTACTTCCC ATAATAATGA CTGATTTATT TGTAATTCAG GTATTTATAA	60
ACCTATTGGC TACAAAGACT TTGTAAACA TTATCCAGTG GTTTTCGTGA AATGGAATTA	120
TGTTTATTTT TATGGGATTT GGGTAAATTT TAAATTGTCT AGAAACTGA AATTTAGTT	180
GTCAGTTGTG GAATTCAGTT TTTCAATTGT GGAAATTTCC TGCCACCCCA ACAGTATTTT	240
TGTGTGTTAA TTAATTTTGC AAAATGAGAA TCATGGTGTG AACTCATCT AATTTATCTT	300
GTTGTGATGT TATGGTCATA ATACGGAGAA AGAGGGTTTA ATTTTCTTG TATTTGGTTT	360
CCTGGTGGTA TCATAGTGTA ATTTTAGTAT TTGAAAATCA GTGTGATTCC TTAATGGCCA	420
ACTGAAGATT GAATTGCCGC TAACAACCAT ATCGTGTTAG TGAATTTTCA ATATGGACCA	480

GGAAGGCATA TGTAATTTGA ACTTGAGTGA AAAGGTTGAA G

521

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AATAGATACA AACTCAATTT TGCATAGAAA GGTATATTTT GAATAGTTCC CATGTTGTGT	60
TCTCACATTA GAGTAATTC TGTATTAAAC CATGAAAATT GCACTTTATG AGTGATACCC	120
ATTTGAGGGC CTCTAAACCC TTCAATTTGG TACTCACGTG AAGAGGGGAAA GCGGAAGATG	180
GTAATTTTTT TTTACGGATG ATATGGCAGG ATGATTGGTT CTGATCTTAC CGGCTAGTGG	240
TCATTTTTTA AAAACTTGTA CCCTCTTATC TGAAATCCTG TTTCTGGAAT TTGGCCATTT	300
TAAGTGATTT TGTTTGGCCT CTTCTATAAT ATTCCTACTT CCCATAATAA TGACTGATTT	360
ATTTGTAATT CAGGTATTTA TAAACCTATT GGCTACAAAG ACTTTGTTAA ACATTATCCA	420
GTGGTTTTTCG TGAAATGGAA TTATGTATAT TTTTATGGGA TTTGGGAAAT TTAAATTGT	480
CTAGAAAAC T GAAATTTTCAG TTGTCAGTTG TGGAATT	517

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACTGTTGG GGTGGCAGGA AATTTCCACA ATTGAAAAAC TGAATTCCAC AACTGACAAC	60
TGAAATTTCA GTTTTCTAGA CAATTTAAAA TTTACCCAAA TCCCATAAAA ATAAACATAA	120
TTCCATTTCA CGAAAACCAC TGGATAATGT TTAACAAAGT CTTTGTAGCC AATAGGTTTA	180
TAAATACCTG AATTACAAAT AAATCAGTCA TTATTATGGG AAGTAGGAAT ATTATAGAAG	240
AGGGCAAACA AAATCACTTA AAATGGCCAA ATTCCAGAAA CAGGATTTC AATAAGAGGG	300
TACAAGTTTT TTAAAAATNG ACCACTAGCC GGTAAGATCA GAACCAATCA TCCTGCCATA	360

TCATCCGTAA AAAAAAATTA CCATCTTCCG CTTTCCCTCT TCACGTGAGT ACCAAATTGG 420
AAGGGGTTAG AGGCCCTCAA ACGGGTATCA CTCATAAAGG CA 462

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTNTAATTAA CACACAAAAA TACTGTTGGG GTGGCAGGAA ATTTCCACAA TTGAAAAACT 60
GAATTCCACA ACTGACAACT GAAATTTTCTAGAC AATTTAAAAT TTACCCAAAT 120
CCCATAAAAA TAAACATAAT TCCATTTTAC GAAACCACT GGATAATGTT TAACAAAGTC 180
TTTGTAGCCA ATAGGTTTAT AAATACCTGA ATTACAAATA AATCAGTCAT TATTATGGGA 240
AGTAGGAATA TTATNGAAGA GGGCAAACAA AATCACTTAA AATGGCCAAA TTCCAGAAAC 300
AGGATTTTCTAG ATAAGAGGGT ACAAGTTTTT TAAAAATGAC CACTAGCCGG TAAGATCAGA 360
ACCAATCATC CTGCCATATC ATCCGTAAAA NAAAATTACC ATCTTCCGCT TTCCCTCTTC 420
ACGTGAGTAC CAAATTGAAG GGTTTAGG 448

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

NGNGGTNNCG TCGGTAAAT ATTCAAGACC AAAGCCAAAG ATCTCTTCAT AGGTGATGTG 60
ATCCACAATG CTGGACCTCA TCGGGATAAG AAGCTGAAGT ACTACATCCC AGAAGTTGTT 120
TACTCTGGCC TCTACCCACC CTATGCAGGG GGAGGGGGGT TCCTCTACTC CGGCCACCTG 180
GCCCTGAGGC TGTACCATAT CACTGACCAG GTCCATCTCT ACCCCATTGA TGACGTTTAT 240
ACTGGAATGT GCCTTCAGAA ACTCGGCCTC GTTCCAGAGA AACACAAAGG CTTCAGGACA 300
TTTGATATCG AGGAGAAAAA CAAAAATAAC ATCTGCTCCT ATGTAGATCT GATGTTAGGA 360

CATAGNAGGA AAACCTCAAG AGATGATTGA TATTTGGGCT CAAGNTGCAG AGTGCTCAAT	420
TTAAATGCT AAAATAGATA CAAACTCAAT TTGGGATTNG AAGGGGTTTT TNGGATTGGC	480
CCCATNTGGG GTCTTNANAT TAGAGNNGGT TCAAGTGGGT ACAGTGATGA AAANNNNNNN	540
NNNNGGNNNN NNNNCCNNNT NNTTNNAANN NNNNNNNNNN NNNNNNNNNN NNTNNCANN	600
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	660
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	720
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	780
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	840
NNNNNNNNNN NNNNNNG	857

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATGATTG ATATTGGTC TCAGTGCAG AGTGCTCATT TAAATGCTA AAATAGATAC	60
AAACTCAATT TTGCATAGAA AGGTGTATTT TGAATAGTTC CCATGTTGTG TTCTCACATT	120
AGAGTAATTT CTGTATTAAA CCATGAAAAT TGCCTTTATG AGTGATACCC ATTTGAGGGC	180
CTCTAAACCC TTCAATTTGG TACTCACGTG AAGAGGGAAA GCGGAAGATG GTAATTTTTT	240
TTTACGGATG ATATGGCAGG ATGATTGGTT CTGATCTTAC CGGCTAGTGG TCATTTTTTAA	300
AAACTTGTG CCCTCTTATC TGAAATCCTG TTTCTGGGAA TTTGGCCATT TTAAGTGATT	360
TTGTTTGCCC TCTTCTATNA ATATTCCTAC TTCCNTAAT AATGACTGAT TTNATTTGTA	420
ANTCAGGNAT TTATNAAACC CTTGGGCTAC CAAGNCTTGT TAAACAT	467

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TACTGTTGGG GTGGCAGGAA ATTTCCAAAA TTGAAAAACT GAATTCCACA ACTGACAACT	60
GAAATTTTCAG TTTTCTAGAC AATTTAAAAAT TTACCCAAAT CCCATAAAAA TAAACATAAT	120
TCCATTTTCAC GAAAACCACT GGATAATGTT TAACAAAGTC TTTGTAGCCA ATAGGTTTAT	180
AAATACCTGA ATTACAAATA AATCAGTCAT TATTATGGGA AGTAGGAATA TTATAGAAGA	240
GGGCAAACAA AATCACTTAA AATGGCCAAA TTCCAGAAAC AGGATTTTCAG ATAAGAGGGT	300
ACAAGTTTTT TAAAAATGAC CACTAGCCCG GTAAGATCAG AACCAATCAT CCTGCCATAT	360
CATCCGTAAA AAAAAATTAC CATCTTCCGC TTTCCCTCTT CACGTGAGTA CCAAATTGGA	420
AGGGGTTAGA GGCCCNCCAA CG	442

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TACTGTTGGG GTCGGCAGGA AATTTCCACA ATTGAAAAAC TGAATTCCAC AACTGACAAC	60
TGAAATTTCA GTTTTCTAGA CAATTTAAAA TTTACCCAAA TCCCATAAAA ATAAACATAA	120
TTCCATTTCA CGAAAACCAC TGGATAATGT TTAACAAAGT CTTTGTAGCC AATAGGTTTA	180
TAAATACCTG AATTACAAAT AAATCAGTCA TTATTATGGG AAGTAGGAAT ATTATACGAA	240
GAGGGCAAAC AAAATCACTT AAAATGGCCA AATTCCAGAA ACAGGATTTC AGATAAGAGG	300
GTACAAGTTT TTTAAAAATG ACCACTAGCC CGGTAAGATC AGAACCAATC ATCCCTGGCC	360
ATATCATCCG GTAAAAAAA ATTACCATCT TCCGCTTTTC CCTCTTCACG TGAGGTACCC	420
AATTGGAANG GGTTTAGAAG GCCCTCAAAC GGGTATCACT CNTTAAAGGC ANTTTCATGG	480
GTTAATATGG AATTACCNCT AATGGTGAGA CCCACCTGG GGACTATTCC AAATACCCCT	540
TCCATGGCAA ATTGGNGTTG GAACCANTTT AGCAT	575

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGATACCCAT TTGAGGGCCT CTAAACCCCTT CAATTTGGTA CTCACGTGAA GAGGGAAAGC	60
GGAAGATGGT AATTTTTTTTT TATGGATGAT ATGGCAGGAT GATTGGTTCT GATCTTACCG	120
GCTAGTGGTC ATTTTTTAAAA AACTTGTAACC CTCTTATCTG AAATCCTGTT TCTGGAATTT	180
GGCCATTTTA AGTGATTTTG TTTGCCCTCT TCTATAATAT TCCTACTTCC CATAATAATG	240
ACTGATTTAT TTGTAATTCA GGTATTTATA AACCTATTGG CTACAAAGAC TTTGTTAAAC	300
ATTATCCAGT GGTTTTTCGTG AAATGGGAAT TATGTTTATT TTTATGGGGA TTTGGGTAAA	360
TTTTAAATTG TCTAGGAAAA CTGAAATTTT CAGTTGTCCA GTTGTGGGAA TTCAGTTTTT	420
CCAATTGTGG GAAATTTCCC GGCCACCCCA ACAGTATTTT TGTGTGGTTA ATTAATTTTT	480
GCCAAATGAG GATCCNGGGT GTGACCACTN T	511

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTAAATTTTA AATTGTCTAG AAAACTGAAA TTTCAGTTGT CAGTTGTGGA ATTCAGTTTT	60
TCAATTGTGG AAATTCCTG CCACCCCAAC AGTATTTTTG TGTGTTAATT AATTTTGCAA	120
AATGAGAATC ATGGTGTGAC ACTCATCTAA TTTATCTTGT TGTGATGTTA TGGTCATAAT	180
AAGGAGAAAG AGGGTTTAAT TTTCTTGTA TTTGGTTTCC TGGTGGTATC ATAGTGTAAT	240
TTTAGTATTT GAAAATCAGT GTGATTCCTT AATGGGCCAA CTGAAGATTG AATTGCCGCT	300
AACAACCATA TCGTGTTAGT GAATTTTCAA TATGGGACCN GGAAGGGCAT ATGTATTTTG	360
GAACTTGGAG TGGAAAAGGT TGGAGTTACA GACTTTTGGC	400

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGAGGGTCAC	GTGCGGTGGTT	ACGGGTTTTA	ACAACTTGCC	GGACAGATTT	AAAGACTTTC	60
TGCTGTATTT	GAGATGCCGC	AATTATTCAC	TGCTTATAGA	TCAGCCGGAT	AAGTGTGCAA	120
AGAAACCTTT	CTTGTTGCTG	GCGATTAAGT	CCCTCACTCC	ACATTTTGCC	AGAAGGCAAG	180
GCAATCCGGG	AATCCTGGGG	CCAAGAAAGC	AACGCAGGGA	ACCAAACGGT	GGTGCGAGTC	240
TTCCTGCTGG	GCCAGACACC	CCCAGAGGAC	AACCACCCCG	ACCTTTCAGA	TATGCTGAAA	300
TTTTGAGAGT	GAGAAGCACC	AAGACATTCT	TATGTGGGAA	CTACAGAGGA	CACTTTCTTT	360
CAANTTGTCT	NTGGAAGGAA	GTGCTGTTTT	TTCAGGTGGG	GTTAAGTTAT	TTCCTGCCCA	420
GACATTGAGT	TTGTTTTTTC	AAGGGGCGAT	GGACGATGTT	TTTGTTGNAC	ACCCTTCACT	480

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTAATTAACA	CACAAAAATA	CTGTTGGGTA	NANNAANAAA	TTCCACAAT	TGAAAACTG	60
AATTCACAA	CTGACAACTG	AAATTTAGT	TTTCTAGACA	ATTTAAAATT	TACCCAAATC	120
CCATAAAAT	AAACATAATT	CCATTTACG	AAAACCACTG	GATAATGTTT	AACAAAGTCT	180
TTGTAGCCAA	TAGGTTTATA	AATACCTGAN	TTACAAATAA	ATCAGTCATT	ATTATGGGAA	240
GTAGGAATAT	TATAGAAGAG	GGCAAACAAA	NTCACTTAAA	ATGGCCAAAT	TCCAGGANAC	300
AGGGATTTC	GATAAGAGGG	TACAAGTNTT	TTAAAAGTGA	CCACTAGGCC	GGGTAAGGTC	360
CGGANCCAAT	CATCCTGCCA	TNTTCATCCG	TA			392

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GNCCCCAGTA TCCCATCTGA TAAGAACCTT CAATTCTATA AACAAAAATA TTTCAAGAAA	60
GTATGTTACA CAATAGTACA TATAAGTAAT AGTTTGGCAG AATTTTAAAC TCTAGTAGTT	120
CATACCCCCA AAAAACAAAT TTTAAAATTC AAAAATAACA GTTTTATTTA ACATATGTTA	180
CACCTTAACA TTTAAAATAT CATGCTCTAG TTAAATATTT CATCAACAAC ACTGTATACA	240
ANTAAAATAT TACATAANAT ATATTTAAGG NAAATGTTTT GGGTCTTTGA TCTGGAACAN	300
TAAATAAAAA CACGGGCACT TCTACATAGG ACGGGGGTGG CGGTTACTAC TCCAATAATA	360
ATCNTGGTNT AGGGCGGCTT G	381

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCAAAGAC CAAAACATTT TCTTAAATAT ATTTTATGTA ATATTTTATT TGTATACAGT	60
GTTGTTGATG AAATATTTAA CTAGAGCATG ATATTTTAAA TGTTAAGGTG TAACATATGT	120
TAAATAAAAC TGTTATTTTN GAATTTNAAA ATTNNGTTTT NGGGGGTATG ANCTACTAGA	180
GTTTAAAATT CTGCCAACT ATTACTTATA TGTNCTATTG TGTAACATAC TTNCTNGAAA	240
TATTTNGGTT TATAGAATTG ANGTTTCTTA TCAGATGGGA TACTGGGGAC TATAACAAT	300
GGAAATAAAG CCACTGTATT TNT	323

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAAATACAG TGGCTTTATT TCCATTGTTT ATAGTCCCCA GTATCCCATC TGATAAGAAC	60
CTTCAATTCT ATAAACAAAA ATATTTCAAG AAAGTATGTT ACACAATAGT ACATATAAGT	120

AATAGTTTGG CAGAATTTTA AACTCTAGTA GTTCATACCC CCAAAAAACA AATTTTAAAN	180
TTCAAAAATA ACAGTTTTTAT TTAACATATG TTACACCTTA ACATTTAAAA TATCATGCTC	240
TAGTTAAATA TTTCATCAAC AACACTGTAT ACANNTAAAA TATTACATAA AATATATTT	299

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACAGATTTA AAGACTTTCT GCTGTATTTG AGATGCCGCA ATTATTCCT GCTTATAGAT	60
CAGCCGGATA AGTGTGCAAA GAAACCTTTC TTGTTGCTGG CGATTAAGTC CCTCACTCCA	120
CATTTTGCCA GAAGGCAAGC AATCCGGGAA TCCTGGGGCC AAGAAAGCAA CGCAGGGAAC	180
CAAACGGTGG TGCGAGTCTT CCTGCTGGGC CAGACACCCC CAGAGGACAA CCACCCCGAC	240
CTTTCAGATA TGCTGAAATT TGAGAGTTAG AAGCACCAAG ACATTCCTTA TGTGGGACCT	300
ACA	303

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTATTTCCA TTGTTTATAG TCCCCAGTAT CCCATCTGAT AAGAACCTTC AATTCTATAA	60
ACAAAAATAT TTCAAGAAAG TATGTTACAC AATAGTACAT ATAAGTAATA GTTTGGCAGA	120
ATTTTAAACT CTAGTAGTTC ATACCCCCAA AAAACAAATT TTAAAATTCA AAAATAACAG	180
TTTTATTTAA CATATGTTAC ACCTTAACAT TTAAATATATC ATGCTCTAGT TAAATATTTT	240
ATCAACAACA CTGTATACAA ATAAATATT ACATAAANTA TATTTAAGGN AAATGTTTTG	300
GGTCTTTGAT CTGGAAC	317

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTAAAAATAN AGTGGCTTTA TTTCCATTGT TTATAGTCCC CAGTATCCCA TCTGATAAGA	60
ACCTTCAATT CTATAAACAA AAATATTTCA AGAAAGTATG TTACACAATA GTACATATAA	120
GTAATAGTTT GGCAGAATTT TAAACTCTAG TAGTTCATAC CCCCACAAAAA CAAATTTTAA	180
AATTCACAAAA TAACAGTTTT ATTTAACATA TGTTACACCT TAACATTTAA AATATCATGC	240
TCTAGGTTAA ATATTTTCATC AACAACACTG GTATACAAAT AAAATATTAC ATAAAAATATA	300
TTTAAGGGAA ATGTTTTGGG GCTTT	325

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTTTGCCAGA AGGCAAGCAA TCCGGGAATC CTGGGGCCAA GAAAGCAACG CAGGGAACCA	60
AACGGTGGTG CGAGTNTTCC TGCTGGGCCA GACACCCCA GAGGACAACC ACCCCGACCT	120
TTCAGATATG CTGAAATTTG AGAGTGAGAA GCACCAAGAC ATTCTTATGT GGAACACAG	180
AGACACTTTN TTCAACTTGT CTCTGAAGGA AGTGCTGTTT CTNAGGTGGG TAAGTACTTC	240
CTGCCCAGAC ACTGAGTTTG TTTTCAAGGG CGATGACGAT GT	282

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AATTTCCACA ATTGAAAAAC TGAATTCAC AACTGACAAC TGAAATTTCA GTTTTCTAGA	60
CAATTTAAAA TTTACCCAAA TCCCATAAAA ATAAACATAA TTCCATTTCA CGAAAACCAC	120
TGGATAATGT TTAACAAAGT CTTTGTAGCC AATAGGTTTA TAAATACCTG AATTACAAAT	180
AAATCAGTCA TTATTATGGG AAGTAGGAAT ATTATAGAAG AGGGCAAACA AAATCACTTA	240
AAATGGCCAA ATTCCAGGAA ACAGGGATTT CAGGATAAGG GGGTACAAGT TTTTAAAAA	300
TGGACCACTA GGCCGGGTAA GGATCAGGAA CCANTTCATC CTGGCCATAT TCATCCGT	358

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACTTCCTGCC CAGACACTGA GTTTGTTTTT AAGGGCGATG ACGATGTTTT TGTGAACACC	60
CATCACATCC TGAATTACTT GAATAGTTTA TCCAAGACCA AAGCCAAAGA TCTCTTCATA	120
GGTGATGTGA TCCACAATGC TGGACCTCAT CGGGATAAGA AGCTGAAGTA CTACATCCCA	180
GAAGTTGTTT ACTCTGGCCT CTACCCACCC TATGCAGGGG GAGGGGGGTT CCTCTACTCC	240
GGCCACCTGG GCCTGAGGCT GTACCATATT CACTGGACCA GGGTCCATCT CTTACCCCAT	300
TGGATGGACG TTTTATACTG GGAATGTGNC CTTCAGGAAA NTCGGGCCTC GTTTCCAGGA	360
GGAAACACAA AGGGTTTCAG GGGACATTTT GATATTCGAG GGGAGGGAAA AACAAAAANT	420
TAACATTT	428

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTTGCCAGA AGGCAAGCAA TCCGGGAATC CTGGGGCCAA GAAAGCAACG CAGGGAACCA	60
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AACGGTGGTG CGAGTNTTCC TGCTGGGCCA GACACCCCA GAGGACAACC ACCCCGACCT	120
TTCAGATATG CTGAAATTTG AGAGTNAGAA GCACCAAGAC ATTCTTATGT GGAACACAG	180
AGACACTTTC TTCAACTTGT CTCTGAAGGA AGTGCTGTTT CTCAGGTGGG TAAGTACTTC	240
CTGCCCAGAC ACTGAGTTTG TTTTCA	266

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTGTTGGGTA TCCTGATGAT GGCAAATGTC TTCATTTATT TTATTATGGA AGTCTCCAAA	60
AGCAGTAGCC AAGAAAAAAA TGGAAAAGGG GAAGTAATAA TACCCAAAGA GAAGTTCTGG	120
AAGATATCTA CCCCTCCCGA GGCATACTNG AACCGAGAGC AAGAGAAGCT GAACCGGCAG	180
TACAACCCCA TCCTGAGCAT GCTGACCAAC CAGACGGGGG AGGCGGGCAG GCTCTCCAAT	240
ATAAGNCATC TGAACACT	259

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTATAGNCCC CAGTATCCCA TCTGATAAGA ACCTTCAATT CTATAAACAA AAATATTTCA	60
AGAAAGTATG TTACACAATA GTACATATAA GNAATAGTTT GGCAGAATTT TAACTCTAG	120
TAGTTCATAC CCCCAAAAAA CAAATTTTAA AATTCAAAAA TAACAGTTTT ATTTAACATA	180
TGTTACACCT TAACATTTAA AATATCATGC TCTNGTTAAA TATTTTCATCA ACAACACTGT	240
ATACAAA	247

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGATGTTAG TACATAGTAG AAAACCTCAA GAGATGATTG ATATTTGGTC TCAGTTGCAG	60
AGTGCTCATT TAAAATGCTA AAATAGATAC AAACCTCAATT TTGCATAGAA AGGTGTATTT	120
TGAATAGTTC CCATGTTGTG TTCTCACATT AGAGTAATTT CTGTATTAAA CCATGAAAAT	180
TGCCTTTTATG AGTGATACCC ATTTGAGGGG CCTCTTAAAC CCTTCAATTT GGGTACTTCA	240
CGTGAAGAGG GGAAAGCGGG AAGATGGGTA ATTTTTTTTTT ACGGGATGGA TATGGGCNNG	300
GATGATTGGG TTCTGGATCC TTACCCGGCC TAGTGGGTCC ATTTTTTAAA AAACCTTGGA	360
CCCCCNCC	368

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AAAAATACAG TGGCTTTTATT TCCATTGTTT ATAGTCCCCA GTATCCCATC TGATAAGAAC	60
CTNCAATTCT ATAAACAAAA ATATTTCAAG AAAGTATGTT ACACAATAGT ACATATAAGT	120
AATAGTTTGG CAGAATTTTA AACTCTAGTA GTTCATACCC CCAAAAAACA AATTTTAAAA	180
TTCAAAAATA ACAGT	195

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GAAATATTTT TGTTTATAGA ATTGAAGGTT CTTATCAGAT GGGATACTGG GGACTATAAA	60
CAATGGAAAT AAAGCCACTG TATTTTTAAT TTTTGTGTA ATGTGTAATC TATAATCCTT	120
TTGTTTCCCA TATTTGAGAA CATTTTTCCC TGAAAGAGGC CAGTTTCCTC CCCAGAAACC	180
ATTACAGTAG TGTTGAACTA TCACTGTCTC TCAGTGCCTC ATCCATCTTT GCATTTAAAA	240
TCCCCAAAGT GCTTTCCCAT TTAAAGTCTT TAAAGAAAAG TGAGAATATT TATTTATGCT	300
TCCATTTTCA GTGAGTATAA ATAATTTAAT TAGGGAGTGG TGTGGCATTG TAAAGATTGT	360
GTTATCCTAA GCCATTTCTA TTTTGGAGTT TGTAGCCACA AAGATGAAAT ATAGAATCAG	420
CCTTGACTAC TCAATTTCCCT TTCATAGACC CATGTTGAGA AGACACTACT AACGTCCAGT	480
GGGAAACAAG TAGACAATTG ATGAAGCTCA AAAAACAGAA GGGTTAGTGT TGTAAGAGCA	540
AACAGTCTAA TCCTGTTTGG AATGTGGAAG CCATTTCTGA GCAAGTATGA GGACACAGGT	600
GCTTGATTTG AGATTGAAGA CTGTTTTCTAG CCTGGTCTTC CTGAAGGTTT CCTGGGGCCT	660
GCATCTGCCT TCTACTCCCA TGGCTGCTAG CACACACCTC CCAGAGGGCC ATATTGCCAC	720
ATTATGGCTA GAGAAGAGTA AAGAAGAAAA GAAGCTCTGA GAACATTAC AGGTAATTGG	780
ATCACATTTG CATTTGTCCA AAAAACCTGA CCACGCATTC TCAGGTAATA GGTTCCTCCT	840
CTCAGAGGAA TTTCAATTTT TTTTCTTGTT AGAGATTCCC CTTCTCTGAG GTTTCAGTC	900
TCTTGTAGAG AAAGAAGAGA TGGAGCAGGT TTTGAATGAG GTGTGGAGGG CCACTGGGGG	960
GCCTTTTGTG AGCCTTCAGT CCACATGTGT GCTGTTGTTT GAACATGAGT TCTTGGTGCT	1020
GATGACATTT GGATGAGATG ATCTCTGGCC CTTCTTCATT TGGCAGAAGT TCTTGTGCAA	1080
TGGCTGCCCA AGCCCACCAC ACTGGTCATT GCTGCCCTGT GAGATGGACC TCATGGGCTT	1140
TTTAGCAGAG CACGTTAGGT TTTAGAGCTT TACGCATGCT TGGGCTCTGT TATGGCGCAA	1200
ACCCTTAAAT CCAGGAAGGC CTCTCTTGGT GCCACAATA TGGGTTCTCA CCTGATCCCC	1260
CATCTCACGG ATGGAAGTGC TGTAAGTCTA ACTTATTCTT TGAGAACTGT TTAACAATTA	1320
GGCCTCAAGG GAAACTGGTA TTTTGGGCCC TTTTCTTGGC TATTCCCAAG TCATGTTGAT	1380
TTTGAGTTTG AAGGTCAAAA AGGCTGAAAG CATTGCCAGG GTTTGGACTA TTCAAAAACC	1440
CAAGCAGGTC TTAAAAAAG GATGCAAGAG ACAAGAATGG CTCATTCCCC TTCCTGATCC	1500
TGTTTATACC CATGTCCTTT CTTGAGATGG TCAAGAGAGG CTGGAAAGAA GAACAGGAAA	1560
TTGGGGGAGT GCTTTGTTAC ACTTGGAAT TGAGTCAAGA ATTAAAGACA CCCAAAGTGG	1620
GCCATCTCCT ACTTGTCAC ACCTGATTGG TGGTGATGCG GAATATTTGA TGTCCCGGGT	1680
CATCTTGACT TTCTCAGATG CAAAAAGGGA GGGTGACTTT ACTAATGGAA AGGATGGGAA	1740
GCTGAAATGA ATGAAGCCTT CAGTTGGGCC AAAGTTTAAC TTCCCCGTGA TTTGCCTTCT	1800
GATGAAAAAT GCCAGATGAA GTGAAAATTC TTGTTTCTTG CCTAGAACAG GAAAATACAT	1860

ACTTTACATG CTGGGCTATT GAGGCTATGA AATTAGGTTT TCCTTAATGT AAATCCAATT	1920
GCTAGAAACA TTGCCAAAT AAGATTTTTT GAACTGAACT TTGTTTGCAT TAATCTGAAA	1980
AACTGAAGTA TTCTGACTCA TGAAGTTCTC AAAGTAATAC ACTAAAAAAG TTTTGCCCTT	2040
AATACCATTA TATCTTGTAG AGGCCAAGAA TGAGGGACTT CTGTCTTTAA AGAGCCCTAA	2100
AAATCTCGTT TGCTCACATG ATATGAATTA CCGTATTTGT TGTAATGCG CAACTTTGTA	2160
TACACTAAAA GCACTGCCAA TATGATTTTT TATCAGTTGT GCCTCAGTTA GAGATATTAA	2220
AATGTGACAT CTTAAATATT ACATATTAGA ATAATTG	2257